

Proline specific permease PUT4 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Proline+specific+permease+PUT4*#gephebase-summary-title)	Gephebase Gene	GP00001501	GepheID
Published	Entry Status	Prigent	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)		Trait Category	
Nitrogen use (growth rate on proline) (https://www.gephebase.org/search-criteria?/and+Trait=^Nitrogen use (growth rate on proline)^#gephebase-summary-title)		Trait	
Budding yeast		Trait State in Taxon A	
Budding yeast West African DBVPG6044 (WA)		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	Latin Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	Latin Name
baker’s yeast	Common Name	baker’s yeast	Common Name
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker’s yeast; S. cerevisiae; brewer’s yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Synonyms	Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker’s yeast; S. cerevisiae; brewer’s yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
Budding yeast (wild strains - see article)	Taxon A Description	Budding yeast West African DBVPG6044 (WA)	Taxon B Description

PUT4	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
	Synonyms	P15380 (http://www.uniprot.org/uniprot/P15380)
YOR348C; O6345	String	GenebankID or UniProtKB M30583.1 (https://www.ncbi.nlm.nih.gov/nucore/M30583.1)
4932.YOR348C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YOR348C)	Sequence Similarities	
Belongs to the amino acid-polyamine-organocation (APC) superfamily. YAT (TC 2.A.3.10) family.		
GO - Molecular Function		
GO:0015193 : L-proline transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015193)		
GO:0015175 : neutral amino acid transmembrane transporter activity		

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015175>)

GO - Biological Process

GO:0015812 : gamma-aminobutyric acid transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015812>)

GO:0015804 : neutral amino acid transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0015804>)

GO:0015824 : proline transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015824>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

several synonymous and promoter mutations

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title>)

Main Reference

Concerted evolution of life stage performances signals recent selection on yeast nitrogen use. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25349282>)

Authors

Ibstedt S; Stenberg S; BagÃ©s S; Gjuvslund AB; Salinas F; Kourtchenko O; Samy JK; Blomberg A; Omholt SW; Liti G; Beltran G; Warringer J

Abstract

Exposing natural selection driving phenotypic and genotypic adaptive differentiation is an extraordinary challenge. Given that an organism’s life stages are exposed to the same environmental variations, we reasoned that fitness components, such as the lag, rate, and efficiency of growth, directly reflecting performance in these life stages, should often be selected in concert. We therefore conjectured that correlations between fitness components over natural isolates, in a particular environmental context, would constitute a robust signal of recent selection. Critically, this test for selection requires fitness components to be determined by different genetic loci. To explore our conjecture, we exhaustively evaluated the lag, rate, and efficiency of asexual population growth of natural isolates of the model yeast *Saccharomyces cerevisiae* in a large variety of nitrogen-limited environments. Overall, fitness components were well correlated under nitrogen restriction. Yeast isolates were further crossed in all pairwise combinations and coinheritance of each fitness component and genetic markers were traced. Trait variations tended to map to quantitative trait loci (QTL) that were private to a single fitness component. We further traced QTLs down to single-nucleotide resolution and uncovered loss-of-function mutations in RIM15, PUT4, DAL1, and DAL4 as the genetic basis for nitrogen source use variations. Effects of SNPs were unique for a single fitness component, strongly arguing against pleiotropy between lag, rate, and efficiency of reproduction under nitrogen restriction. The strong correlations between life stage performances that cannot be explained by pleiotropy compellingly support adaptive differentiation of yeast nitrogen source use and suggest a generic approach for detecting selection.

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Additional References

RELATED GEPHE

Related Genes

3 (Allantoin permease DAL4, Allantoinase DAL1, Serine/threonine protein kinase RIM15) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Nitrogen use/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

PUT4 encoding a high-affinity proline permease